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## RAW SEQUENCE LISTING

DATE: 10/16/2001

PATENT APPLICATION: US/09/964,667

TIME: 15:24:03

Input Set : A:\PTO.txt

Output Set: N:\CRF3\10162001\I964667.raw

## SEQUENCE LISTING

## 4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: de la Monte, Suzanne  
7 Wands, Jack R.

9 (ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for  
10 Screening Drugs Effective for the Treatment or Prevention  
11 of Alzheimer's Disease

13 (iii) NUMBER OF SEQUENCES: 14

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

17 (B) STREET: 1100 New York Ave., Suite 600

18 (C) CITY: Washington

19 (D) STATE: DC

20 (E) COUNTRY: USA

21 (F) ZIP: 20005-3934

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/964,667 dv

C--> 31 (B) FILING DATE: 28-Sep-2001

32 (C) CLASSIFICATION:

34 (viii) ATTORNEY/AGENT INFORMATION:

35 (A) NAME: Esmond, Robert W.

36 (B) REGISTRATION NUMBER: 32,893

37 (C) REFERENCE/DOCKET NUMBER: 0609.4370000

39 (ix) TELECOMMUNICATION INFORMATION:

40 (A) TELEPHONE: 202-371-2600

41 (B) TELEFAX: 202-371-2540

44 (2) INFORMATION FOR SEQ ID NO: 1:

46 (i) SEQUENCE CHARACTERISTICS:

47 (A) LENGTH: 1442 base pairs

48 (B) TYPE: nucleic acid

49 (C) STRANDEDNESS: double

50 (D) TOPOLOGY: both

52 (ii) MOLECULE TYPE: cDNA

55 (ix) FEATURE:

56 (A) NAME/KEY: CDS

57 (B) LOCATION: 15..1139

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

62 TTTT TTTT TGAG ATG GAG TTT TCG CTC TTG TTG CCC AGG CTG GAG TGC 50

63 Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys

64 1 5 10

66 AAT GGC GCA ATC TCA GCT CAC CGC AAC CTC CGC CTC CCG GGT TCA AGC 98

67 Asn Gly Ala Ile Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser

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68	15	20	25	
70	GAT TCT CCT GCC TCA GCC TCC CCA GTA GCT GGG ATT ACA GGC ATG TGC	146		
71	Asp Ser Pro Ala Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys			
72	30 35 40			
74	ACC CAC GCT CGG CTA ATT TTG TAT TTT TTT TTA GTA GAG ATG GAG TTT	194		
75	Thr His Ala Arg Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe			
76	45 50 55 60			
78	CTC CAT GTT GGT CAG GCT GGT CTC GAA CTC CCG ACC TCA GAT GAT CCC	242		
79	Leu His Val Gly Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro			
80	65 70 75			
82	TCC GTC TCG GCC TCC CAA AGT GCT AGA TAC AGG ACT GGC CAC CAT GCC	290		
83	Ser Val Ser Ala Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala			
84	80 85 90			
86	CGG CTC TGC CTG GCT AAT TTT TGT GGT AGA AAC AGG GTT TCA CTG ATG	338		
87	Arg Leu Cys Leu Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met			
88	95 100 105			
90	TGC CCA AGC TGG TCT CCT GAG CTC AAG CAG TCC ACC TGC CTC AGC CTC	386		
91	Cys Pro Ser Trp Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu			
92	110 115 120			
94	CCA AAG TGC TGG GAT TAC AGG CGT GCA GCC GTG CCT GGC CTT TTT ATT	434		
95	Pro Lys Cys Trp Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile			
96	125 130 135 140			
98	TTA TTT TTT TTA AGA CAC AGG TGT CCC ACT CTT ACC CAG GAT GAA GTG	482		
99	Leu Phe Phe Leu Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val			
100	145 150 155			
102	CAG TGG TGT GAT CAC AGC TCA CTG CAG CCT TCA ACT CCT GAG ATC AAG	530		
103	Gln Trp Cys Asp His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys			
104	160 165 170			
106	CAT CCT CCT GCC TCA GCC TCC CAA GTA GCT GGG ACC AAA GAC ATG CAC	578		
107	His Pro Pro Ala Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His			
108	175 180 185			
110	CAC TAC ACC TGG CTA ATT TTT ATT TTT ATT TTT AAT TTT TTG AGA CAG	626		
111	His Tyr Thr Trp Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln			
112	190 195 200			
114	AGT CTC AAC TCT GTC ACC CAG GCT GGA GTG CAG TGG CGC AAT CTT GGC	674		
115	Ser Leu Asn Ser Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly			
117	205 210 215 220			
119	TCA CTG CAA CCT CTG CCT CCC GGG TTC AAG TTA TTC TCC TGC CCC AGC	722		
120	Ser Leu Gln Pro Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser			
121	225 230 235			
123	CTC CTG AGT AGC TGG GAC TAC AGG CGC CCA CCA CGC CTA GCT AAT TTT	770		
124	Leu Leu Ser Ser Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe			
125	240 245 250			
127	TTT GTA TTT TTA GTA GAG ATG GGG TTC ACC ATG TTC GCC AGG TTG ATC	818		
128	Phe Val Phe Leu Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile			
129	255 260 265			
131	TTG ATC TCT GGA CCT TGT GAT CTG CCT GCC TCG GCC TCC CAA AGT GCT	866		
132	Leu Ile Ser Gly Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala			
133	270 275 280			

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135 GGG ATT ACA GGC GTG AGC CAC CAC GCC CGG CTT ATT TTT AAT TTT TGT      914
136 Gly Ile Thr Gly Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys
137 285                      290                      295                      300
139 TTG TTT GAA ATG GAA TCT CAC TCT GTT ACC CAG GCT GGA GTG CAA TGG      962
140 Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp
141                      305                      310                      315
143 CCA AAT CTC GGC TCA CTG CAA CCT CTG CCT CCC GGG CTC AAG CGA TTC      1010
144 Pro Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe
145                      320                      325                      330
147 TCC TGT CTC AGC CTC CCA AGC AGC TGG GAT TAC GGG CAC CTG CCA CCA      1058
148 Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro
149                      335                      340                      345
151 CAC CCC GCT AAT TTT TGT ATT TTC ATT AGA GGC GGG GTT TCA CCA TAT      1106
152 His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr
153                      350                      355                      360
155 TTG TCA GGC TGG TCT CAA ACT CCT GAC CTC AGG TGACCCACCT GCCTCAGCCT      1159
156 Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg
157 365                      370                      375
159 TCCAAAGTGC TGGGATTACA GCGGTGAGCC ACCTCACCCA GCCGGCTAAT TTAGATAAAA      1219
161 AAATATGTAG CAATGGGGGG TCTTGCTATG TTGCCCAGGC TGGTCTCAA CTTCTGGCTT      1279
163 CATGCAATCC TTCCAAATGA GCCACAACAC CCAGCCAGTC ACATTTTTTA AACAGTTACA      1339
165 TCTTTATTTT AGTATACTAG AAAGTAATAC AATAAACATG TCAAACCTGC AAATTCAGTA      1399
167 GTAACAGAGT TCTTTTATAA CTTTAAACA AAGCTTTAGA GCA                      1442
170 (2) INFORMATION FOR SEQ ID NO: 2:
172     (i) SEQUENCE CHARACTERISTICS:
173         (A) LENGTH: 375 amino acids
175         (B) TYPE: amino acid
176         (D) TOPOLOGY: linear
178     (ii) MOLECULE TYPE: protein
180     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
182 Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys Asn Gly Ala Ile
183   1                      5                      10                      15
185 Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser Asp Ser Pro Ala
186                      20                      25                      30
188 Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys Thr His Ala Arg
189                      35                      40                      45
191 Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly
192                      50                      55                      60
194 Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala
195  65                      70                      75                      80
197 Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys Leu
198                      85                      90                      95
200 Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met Cys Pro Ser Trp
201                      100                     105                     110
203 Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu Pro Lys Cys Trp
204                      115                     120                     125
206 Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile Leu Phe Phe Leu
207                      130                     135                     140
209 Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val Gln Trp Cys Asp

```

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```

210 145          150          155          160
212 His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys His Pro Pro Ala
213          165          170          175
215 Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His His Tyr Thr Trp
216          180          185          190
218 Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln Ser Leu Asn Ser
219          195          200          205
221 Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly Ser Leu Gln Pro
222          210          215          220
224 Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser Leu Leu Ser Ser
225 225          230          235          240
227 Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe Phe Val Phe Leu
228          245          250          255
230 Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile Leu Ile Ser Gly
231          260          265          270
233 Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly
234          275          280          285
236 Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys Leu Phe Glu Met
237          290          295          300
239 Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp Pro Asn Leu Gly
240 305          310          315          320
242 Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe Ser Cys Leu Ser
243          325          330          335
245 Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro His Pro Ala Asn
246          340          345          350
248 Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr Leu Ser Gly Trp
249          355          360          365
251 Ser Gln Thr Pro Asp Leu Arg
252          370          375

```

254 (2) INFORMATION FOR SEQ ID NO: 3:

256 (i) SEQUENCE CHARACTERISTICS:

257 (A) LENGTH: 1381 base pairs

258 (B) TYPE: nucleic acid

259 (C) STRANDEDNESS: double

260 (D) TOPOLOGY: both

262 (ii) MOLECULE TYPE: cDNA

267 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

269 TTTTTTTTTT GAGATGGAGT TTTCGCTCTT GTTGCCCAGG CTGGAGTGCA ATGGCGCAAT      60
271 CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC      120
273 AGTAGCTGGG ATTACAGGCA TGTGCACCAC GCTCGGCTAA TTTTGTATTT TTTTATTAGTA      180
275 GAGATGGAGT TTAACCTCCAT GTTGGTCAGG CTGGTCTCGA ACTCCCGACC TCAGATGATC      240
277 TCCCGTCTCG GCCTGCCCAA AGTGCTGAGA TTACAGGCAT GAGCCACCAT GCCCGGCCCTC      300
279 TGCCTGGCTA ATTTTGTGG TAGAAACAGG GTTTCACCTGA TGGTGCCCAA GCTGGTCTCC      360
281 TGAGCTCAAG CAGTCCACCT GCCTCAGCCT CCCAAAGTGC TGGGATTACA GGCGTCAGCC      420
283 GTGCCTGGCC TTTTATTTT ATTTTCTTGA AGACACAGGT GTACCACTCT TACCCAGGAT      480
285 GAAGTGCAGT GGTGTGATCA CAGCTCACTG CAGCCTTCAA CTCCTGAGAT CAAGCAATCC      540
287 TCCTGCCTCA GCCTCCCAA TAGCTGGGAC CAAAGACATG CACCACTACA CCTGGTAATT      600
289 TTTATTTTTA TTTTAAATTT TTTGAGACAG AGTCTCACTC TGTCACCCAG GCTGGAGTGC      660
291 AGTGGCGCAA TCTTGGCTCA CTGCAACCTC TGCCTCCCGG GTTCAAGTTA TTCTCCTGCC      720

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293 CCAGCCTCCT GAGTAGCTGG GACTACAGGC GCCCACCACG CCTAGCTAAT TTTTTTGTAT 780
295 TTTTAGTAGA GATGGGGTTT CACCATGTTT GCCAGGTTGA TCTTGATCTC TTGACCTTGT 840
297 GATCTGCCTG CCTCGGCCCTA CCCAAAGTGC TGGGATTACA GGTCGTGACT CCACGCCGGC 900
299 CTATTTTAA TTTTGTGTTT TTTGAAATGG AATCTCACTC TGTTACCCAG GTCGGAGTGC 960
301 AATGGCAAAT CTCGGCTACT CGCAACCTCT GCCTCCCGGG TCAAGCGATT CTCCTGTCTC 1020
303 AGCCTCCCAA GCAGCTGGGA TTACGGGACC TGCACCACAC CCCGCTAATT TTTGTATTTT 1080
305 CATTAGAGGC GGGTTTACCA TATTTGTCAG GCTGGGTCTC AAACCTCTGA CCTCAGGTGA 1140
307 CCCACCTGCC TCAGCCTTCC AAAGTGCTGG GATTACAGGC GTGAGCCACC TCACCCAGCC 1200
309 GGCTAATTTT GAAATAAAAA TATGTAGCAA TGGGGGTCTG CTATGTTGCC CAGGCTGGTC 1260
311 TCAAACCTCT GGCTTCAGTC AATCCTTCCA AATGAGCCAC AACACCCAGC CAGTCACATT 1320
313 TTTTAAACAG TTACATCTTT ATTTTAGTAT ACTAGAAAGT AATACAATAA ACATGTCAAA 1380
315 C 1381

```

317 (2) INFORMATION FOR SEQ ID NO: 4:

319 (i) SEQUENCE CHARACTERISTICS:

320 (A) LENGTH: 1418 base pairs

321 (B) TYPE: nucleic acid

322 (C) STRANDEDNESS: both

323 (D) TOPOLOGY: both

325 (ii) MOLECULE TYPE: cDNA

330 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

332 TTTTTTTTTT GAGATGGAGT TTTCGCTCTT GTTGCCAGG CTGGAGTGCA ATGGCGCAAT 60
334 CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC 120
336 AGTAGGCTGG GATTACAGGC ATGTGCACCA CGCTCGGCTA ATTTTGTATT TTTTTTTAGT 180
338 AGAGATGGAG TTTCTCCATG TTGGTCAGGC TGGTCTCGAA CTCCGACCTC AGATGATCCT 240
340 CCCGTCTCGG CCTCCCAAAG TGCTAGATAC AGGACTGAGC ACCATGCCCC GCCTCTGCCT 300
342 GGCTAATTTT TGTGGTAGAA ACAGGGTTTC ACTGATGTGC CCAAGCTGGT CTCCTGAGCT 360
344 CAAGCAGTCC ACCTGCCTCA GCCTCCCAA GTGCTGGGAT TACAGGCGT CAGCCGTGCC 420
346 TGGCCTTTT ATTTTATTTT TTTTAAGACA CAGGTGTCCC ACTCTTACCC AGGATGAAGT 480
349 GCAGTGGTGT GATCACAGCT CACTGCAGCC TTCAACTCTG AGATCAAGCA TCCTCCTGCC 540
351 TCAGCCTCCC AAAGTAGCTG GGACCAAAGA CATGCACCAC TACACCTGGC TAATTTTTTAT 600
353 TTTTATTTTT AATTTTTTTGA GACAGAGTCT CAACTCTGTC ACCCAGGCTG GAGTGCAGTG 660
355 GCGCAATCTT GGCTCACTGC AACCTCTGCC TCCCGGGTTC AAGTTATTCT CCTGCCCCAG 720
357 CCTCCTGAGT AGCTGGGACT ACAGGCGCCC ACCACGCTA GCTAATTTTT TTGTATTTTT 780
359 AGTAGAGATG GGGTTTCACC ATGTTTCGCC GGTGATGCT AGATCTCTTG ACCTTGATGAT 840
361 CTGCCTGCCT CGGCCTCCCA AAGTGCTGGG ATTACAGGAC GTGACGCCCA CCGCCCGGCC 900
363 TATTTTAAAT TTTTGTGTTG TTGAAATGGA ATCTCACTCT GTTACCCAGG CTGGAGTGCA 960
365 ATGGCCAAAT CTCGGCTCAC TGCAACCTCT GCCTCCCGGG CTCAAGCGAT TCTCCTGTCT 1020
367 CAGCCTCCCA AGCAGCTGGG ATTACGGGCA CCTGCACCAC ACCCGCTAA TTTTGTATT 1080
369 TTCATTAGAG GCGGGGTTTC ACCATATTTT TCAGGCTGGT CTCAAACCTC TGACCTCAGG 1140
371 TGACCCACCT GCCTCAGCCT TCCAAAGTGC TGGGATTACA GGCGTGACGC CTCACCCAGC 1200
373 CGGCTAATTT AGATAAAAAA ATATGTAGCA ATGGGGGGTC TTGCTATGTT GCCCAGGCTG 1260
375 GTCTCAAAC TCTGGCTTCA TGCAATCCTT CCAAATGAGC CACAACACCC AGCCAGTCAC 1320
377 ATTTTAAAC AGTTACATCT TTATTTTAGT ATACTAGAAA GTGATACGAT AACATGGCGG 1380
379 AACCTGCAAA TTCGAGTAGT ACAGAGTCTT TTATAACT 1418

```

381 (2) INFORMATION FOR SEQ ID NO: 5:

383 (i) SEQUENCE CHARACTERISTICS:

384 (A) LENGTH: 22 base pairs

385 (B) TYPE: nucleic acid

386 (C) STRANDEDNESS: single

VERIFICATION SUMMARY

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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]